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Oral Communication Abstract – 6.05

A COMMON SET OF GENES RESPONDING TO FLORIGENIC AND PHOTOPERIODIC INDUCTION AT THE SHOOT APICAL MERISTEM OF RICE

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Rice (*Oryza sativa*) is a staple food which is responsible for feeding half of the world, especially in developing countries. The growth in the population and the upcoming climate crisis call for a change in the way we grow our food, and this is were gene editing comes to help.

Rice is a facultative short-day (SD) plant that, coherently with it being a tropical plant, flowers when the days are shorter than a certain threshold, but it can also flower under longer days (LD) if given more time. The molecules essential for this process are the florigens, small globular proteins that carry the flowering signal from the leaves, where they are transcribed and translated, to the shoot apical meristem (SAM), where they trigger the transcription of floral identity genes such as *OsMADS14*, *15*, *18* and *34* (*PAP2*). Rice florigens are Hd3a and RFT1, homologues of *Arabidopsis thaliana* FT. Their action is mostly redundant, but Hd3a is predominantly responsible for flowering in SD, while RFT1 in LD.

To elucidate other possible differences, and how much their action contributes to the flowering induction in the whole photoperiodic frame, we created an inducible system able to express only one florigen (either Hd3a or RFT1) in non-inductive LD conditions when the plant is exposed to a user-administered chemical (dexamethasone DEX).

We then performed three independent RNA-seq experiments, two comparing the transcriptome of DEX-treated plants (expressing either Hd3a or RFT1) with that of mock-treated plants, and the third one comparing the transcriptome of plants in SD inductive to that of plants in LD non-inductive conditions.

We found set of genes which were peculiar of each experiment, together with many genes which were shared between two, or even among all three datasets. We focused on the latter set, composed of 16 genes and we could confirm the dependence on florigens of all uncharacterized genes as their induction was reduced in single *hd3a* or *rft1* or in the double *hd3a rft1* mutant.

To evaluate the importance of some of the uncharacterized target genes, we generated CRISPR-edited plants of one of them. We chose an F-BOX domain protein that we then named *BROADER TILLER ANGLE 1* (*BRT1*) after its functional characterization. We produced two sets of *brt1* mutants: null mutants where a stop codon at the N-term was created and dC mutants where a frameshift was created at the C-term of the protein. Independent alleles in both set of mutants showed widening of the tillers suggesting a role for BRT1 in linking the florigenic signaling to the tiller angle.